

## **Amendments to the Claims**

Please cancel claims 1-17, 29-38, 41-43, 107-108.

1-17 (Cancelled)

18. (Original) A method for determining the function of a sequence alteration in a target up-stream regulatory gene comprising the steps of:

preparing a reference sample from reference cells having a wild-type up-stream regulatory gene corresponding to said target up-stream regulatory gene;

preparing a target sample from target cells having said target up-stream regulatory gene, said target up-stream regulatory gene having said sequence alteration and said target cells being otherwise substantially similar to said reference cells;

detecting the expression of a plurality of down-stream genes in said reference sample to obtain a wild-type expression pattern, said down-stream genes being up or down regulated by said up-stream regulatory gene;

detecting the expression of said plurality of down-stream genes in said target sample to obtain a target expression pattern; and

comparing said reference expression patterns with said target expression pattern to determine the regulatory function of said sequence alteration.

19. (Original) The method of claim 18, wherein said down-stream genes are transcriptionally regulated by said up-stream regulatory gene and said reference and target expression patterns are detected by measuring the amount of transcripts of said down-stream genes in said reference and target samples.

20. (Original) The method of claim 19, wherein said amount of transcripts is detected with a high density nucleic acid array.

21. (Original) The method of claim 18, wherein said reference and target expression patterns are detected by measuring the amount of protein product of said down-stream genes in said reference and target samples.

22. (Original) The method of claim 18 further comprising the steps of:

detecting expression of a plurality of control genes in said reference and target sample, said control genes being unresponsive to the function of said up-stream regulatory gene; and

comparing reference and target expression patterns of control genes to provide a baseline for detecting a significant difference in expression patterns.

23. (Original) The method of claim 18 further comprising the steps of:

a) indicating that said sequence alteration is a loss of function mutation in said target gene if a significant portion of said down regulated genes are expressed relatively higher in said target sample than in said reference sample or if a significant portion of said up-regulated genes are expressed relatively lower in said target sample than in said reference sample;

b) indicating that said sequence alteration is a gain of function mutation in said target gene if a significant portion of said down regulated genes are expressed relatively lower in said target sample than in said reference sample or if a significant portion of said up-regulated genes are expressed relatively higher in said target sample than in said reference sample; and

c) indicating that said sequence alteration is a non functional polymorphism if said reference and target expression patterns are substantially similar.

24. (Original) The method of claim 3, wherein said steps (a), (b) and (c) are performed using a digital computer.

25. (Original) A method for determining genetic regulatory function of a target gene in a target cell type comprising the steps of:

preparing a reference sample from said target cell type having an expressed gene product of said target gene;

blocking the expression of said target gene in said target cell type to prepare a lack-of-function sample;

detecting the expression of at least 2,000 genes in said reference sample and in said lack-of-function sample to obtain a reference and lack-of-function expression pattern; and

comparing said reference expression pattern with said lack-of-function expression pattern to determine the regulatory function of said target gene.

26. (Original) The method of claim 25, wherein said reference and lack-of-function expression patterns are detected by measuring the amount of transcripts of said down-stream genes in said reference and target samples.

27. (Original) The method of claim 26, wherein said amount of transcripts is detected with a high density nucleic acid array.

28. (Original) The method of claim 25, wherein the expression of said target gene is blocked in said loss of function assay by introducing an antisense oligonucleotide.

29-38 (Cancelled)

39. (Original) A device for detecting a functional mutation in a target regulatory gene comprising a high density. nucleic acid array, said nucleic acid array comprising sequences complementary to subsequences of a plurality of down-stream regulatory genes, said regulatory genes being up or down regulated by a wild-type gene corresponding to said target regulatory gene.

40. (Original) A device for detecting a functional mutation in a target regulatory gene comprising a high density. nucleic acid array, said nucleic acid array comprising sequences complementary to subsequences of a plurality of down-stream regulatory genes, said regulatory genes being up or down regulated by a wild-type gene corresponding to said target regulatory gene.

41-43 (Cancelled)

44. (Original) A method for analyzing gene expression data in a computer comprising:

inputting a plurality of expression data reflecting the expression of at least 5 genes in a plurality of biological samples;

correlating said expression data among said genes;

analyzing said correlation to define a regulatory relationship among said genes.

45. (Original) A method for detecting a mutation in a target gene using a computer comprising:

inputting target expression data of a plurality of genes in a target sample containing said target gene, said genes being regulated by said target gene;

inputting wild-type expression data of said plurality of genes in a wild-type sample containing a wild-type gene corresponding to said target gene;

comparing the target and wild-type expression data to detect mutation in said target gene.

46. (Original) A method of determining loss of function of a nucleic acid encoding a regulatory molecule in a test cell comprising:

selecting a first nucleic acid molecule encoding a regulatory molecule;

selecting a set of second nucleic acid molecules whose expression is induced or repressed by the regulatory molecule in normal cells;

hybridizing a transcription indicator of a test cell to a set of nucleic acid probes, wherein the transcription indicator is selected from the group consisting of mRNA, cDNA and cRNA, wherein each member of the set of nucleic acid probes comprises a portion of a nucleic acid molecule which is a member of the set of second nucleic acid molecules;

detecting the amount of transcription indicator which hybridizes to each of said set of nucleic acid probes;

identifying a test cell as having lost function of the regulatory molecule if (1) hybridization of the transcription indicator of the test cell to a probe which comprises a portion of a nucleic acid which is induced by the regulatory molecule is lower than hybridization using a transcription indicator from a normal cell, or (2) hybridization of the transcription indicator of the test cell to a probe which comprises a portion of a nucleic acid which is repressed by the regulatory molecule is higher than hybridization using a transcription indicator from a normal cell.

47. (Original) The method of claim 46 wherein the regulatory molecule is p53.

48. (Original) The method of claim 46 wherein the test cell is a breast cell.
49. (Original) The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 4 genes which are activated or repressed by p53.
50. (Original) The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 10 genes which are activated or repressed by p53.
51. (Original) The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 20 genes which are activated or repressed by p53.
52. (Original) The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 30 genes which are activated or repressed by p53.
53. (Original) The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 100 genes which are activated or repressed by p53.
54. (Original) The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 250 genes which are activated or repressed by p53.
55. (Original) The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 300 genes which are activated or repressed by p53.

56. (Original) The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 400 genes which are activated or repressed by p53.

57. (Original) The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 500 genes which are activated or repressed by p53.

58. (Original) The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 750 genes which are activated or repressed by p53.

59. (Original) The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 1000 genes which are activated or repressed by p53.

60. (Original) The method of claim 46 wherein the nucleic acids which each comprise a portion of a gene which is activated or repressed by p53 are selected from those shown in Table 3.

61. (Original) The method of claim 46 wherein the nucleic acid probes are attached to a solid support.

62. (Original) The method of claim 46 wherein the nucleic acid probes are arranged in an array.

63. (Original) The method of claim 62 wherein the array comprises nucleic acid probes which are portions of at least 250 genes which are either p53-induced or p53-repressed.

64. (Original) The method of claim 62 wherein the array comprises nucleic acid probes which are portions of at least 6000 different genes.

65. (Original) The method of claim 46 wherein at least one of the nucleic acid probes comprises a portion of each of: Cyclin G, GADD45, IGF-BP3, p21<sup>WAF1/CIP1</sup>, Thrombospondin, C-myc, and PCNA, as defined in Table 2.

66. (Original) The method of claim 46 wherein at least one of the nucleic acid probes comprises a portion of each of: Bax, Cyclin G, GADD45, IGF-BP3, p21<sup>WAF1/CIP1</sup>, Thrombospondin, C-myc, and PCNA, as defined in Table 2.

67. (Original) The method of claim 46 further comprising the step of:

determining the sequence of p53 genes in the test cell to confirm the p53 status of the cell.

68. (Original) The method of claim 46 wherein a test cell is identified as p53-negative if hybridization is at least 3-fold different between compared samples.

69. (Original) The method of claim 46 wherein a test cell is identified as p53-negative if hybridization is at least 5-fold different between compared samples.

70. (Original) The method of claim 46 wherein a test cell is identified as p53-negative if hybridization is at least 10-fold different between compared samples.

71. (Original) A method of diagnosing neoplasia of a test cell comprising:

hybridizing a transcription indicator of a test cell to a set of nucleic acid probes, wherein the transcription indicator is selected from the group consisting of mRNA, cDNA and cRNA, wherein the set of nucleic acid probes comprises at least one nucleic acid molecule which is a portion of a gene which is activated by or repressed by p53;

detecting the amount of transcription indicator which hybridizes to each of said set of nucleic acid probes;



identifying a test cell as neoplastic if (1) hybridization of the transcription indicator of the test cell to a probe which is a p53-activated gene is lower than hybridization using a transcription indicator from a normal cell, or (2) hybridization of the transcription indicator of the test cell to a probe which a p53-repressed gene is higher than hybridization using a transcription indicator from a normal cell.

72. (Original) The method of claim 71 wherein the test cell is a breast cell.

73. (Original) The method of claim 71 wherein at least 4 of said probes comprise portions of genes which are p53-activated or p53-repressed.

74. (Original) The method of claim 71 wherein at least 10 of said probes comprise portions of genes which are p53-activated or p53-repressed.

75. (Original) The method of claim 71 wherein at least 20 of said probes comprise portions of genes which are p53-activated or p53-repressed.

76. (Original) The method of claim 71 wherein at least 30 of said probes comprise portions of genes which are p53-activated or p53-repressed.

77. (Original) The method of claim 71 wherein at least 50 of said probes comprise portions of genes which are p53-activated or p53-repressed.

78. (Original) The method of claim 71 wherein at least 75 of said probes comprise portions of genes which are p53-activated or p53-repressed.

79. (Original) The method of claim 71 wherein at least 100 of said probes comprise portions of genes which are p53-activated or p53-repressed.

80. (Original) The method of claim 71 wherein at least 250 of said probes comprise

portions of genes which are p53-activated or p53-repressed.

81. (Original) The method of claim 71 wherein at least 300 of said probes comprise portions of genes which are p53-activated or p53-repressed.

82. (Original) The method of claim 71 wherein at least 500 of said probes comprise portions of genes which are p53-activated or p53-repressed.

83. (Original) The method of claim 71 wherein at least 750 of said probes comprise portions of genes which are p53-activated or p53-repressed.

84. (Original) The method of claim 71 wherein at least 1000 of said probes comprise portions of genes which are p53-activated or p53-repressed.

85. (Original) The method of claim 71 wherein the nucleic acid probes are attached to a solid support.

86. (Original) The method of claim 71 wherein the nucleic acid probes are arranged in an array.

87. (Original) The method of claim 86 wherein the array comprises nucleic acid probes which are portions of at least 250 different genes.

88. (Original) The method of claim 71 wherein the array comprises nucleic acid probes which are portions of at least 6000 different genes.

89. (Original) The method of claim 71 wherein at least one of the nucleic acid probes comprises a portion of each of: Bax, Cyclin G, GADD45, IGF-BP3, p21<sup>WAF1/CIP1</sup>, Thrombospondin, C-myc, and PCNA, as defined in Table 2.

90. (Original) The method of claim 71 wherein at least one of the nucleic acid probes

comprises a portion of each of: Bax, Cyclin G, GADD45, IGF-BP3, p21<sup>WAF1/CIP1</sup>, Thrombospondin, C-myc, and PCNA, as defined in Table 2.

91. (Original) The method of claim 71 further comprising the step of:

determining the sequence of p53 genes in the test cell to determine the p53 genotypic status of the cell.

92. (Original) The method of claim 71 wherein a test cell is identified as neoplastic if hybridization is at least 3-fold different between compared samples.

93. (Original) The method of claim 71 wherein a test cell is identified as neoplastic if hybridization is at least 5-fold different between compared samples.

94. (Original) The method of claim 71 wherein a test cell is identified as neoplastic if hybridization is at least 10-fold different between compared samples.

95. (Original) A method of identifying anti-cancer drugs', comprising the step of:

selecting a protein whose mRNA is induced in tumor cells;

contacting a test compound with the selected protein;

identifying a test compound as a potential anti-cancer drug if it inhibits activity of said protein.

96. (Original) The method of claim 95 wherein the mRNA is induced in breast tumors.

97. (Original) The method of claim 95 wherein the mRNA is induced in BT-474 breast tumor cells.

98. (Original) The method of claim 95 wherein the mRNA is selected from those shown in Table 3.

99. (Original) A solid support comprising an array of nucleic acid probes, wherein at least 50 of said probes comprise a portion of at least 9 contiguous nucleotides of a gene identified in Table 3.

100. (Original) The solid support of claim 99 wherein at least 75 of said probes comprise a portion of at least 9 contiguous nucleotides of a gene identified in Table 3.

101. (Original) The solid support of claim 99 wherein at least 100 of said probes comprise a portion of at least 9 contiguous nucleotides of a gene identified in Table 3.

102. (Original) The solid support of claim 99 wherein at least 150 of said probes comprise a portion of at least 9 contiguous nucleotides of a gene identified in Table 3.

103. (Original) The solid support of claim 99 wherein at least 200 of said probes comprise a portion of at least 9 contiguous nucleotides of a gene identified in Table 3.

104. (Original) The solid support of claim 99 wherein at least 250 of said probes comprise a portion of at least 9 contiguous nucleotides of a gene identified in Table 3.

105. (Original) The solid support of claim 99 wherein at least 300 of said probes comprise a portion of at least 9 contiguous nucleotides of a gene identified in Table 3.

106. (Original) The solid support of claim 99 comprising probes selected from those shown in Table 2.

107-108 (Cancelled)

109. (Original) A method of identifying anti-cancer drugs, comprising the steps of:

contacting a test compound with a tumor cell;

monitoring expression of at least 10 mRNAs which are induced or repressed in tumor cells relative to normal cells;

identifying a test compound as a potential anti-cancer drug if it reduces the amount of at least one mRNA which is induced in tumor cells or enhances the amount of at least one mRNA which is repressed in tumor cells.

110. (Original) The method of claim 109 wherein expression of at least 50 of said mRNAs is monitored.

111. (Original) The method of claim 109 wherein expression of at least 75 of said mRNAs is monitored.

112. (Original) The method of claim 109 wherein expression of at least 100 of said mRNAs is monitored.

113. (Original) The method of claim 109 wherein expression of at least 150 of said mRNAs is monitored.

114. (Original) The method of claim 109 wherein expression of at least 200 of said mRNAs is monitored.

115. (Original) The method of claim 109, wherein expression is measured with high density nucleic acid array.

116. (Original) A method of determining developmental stage of cells or tissues, comprising the steps of:

monitoring in a test sample comprising cells, expression of at least 10 mRNAs which are differentially expressed in cells of different developmental stages;

determining developmental stage of the cells of the test sample by matching the patterns of expression of the at least 10 mRNAs to a reference pattern determined for at least two developmental stages.

117. (Original) The method of claim 116 wherein expression of at least 50 of said mRNAs is monitored.

118. (Original) The method of claim 116 wherein expression of at least 75 of said mRNAs is monitored.

119. (Original) The method of claim 116 wherein expression of at least 100 of said mRNAs is monitored.

120. (Original) The method of claim 116 wherein expression of at least 150 of said mRNAs is monitored.

121. (Original) The method of claim 116 wherein expression of at least 200 of said mRNAs is monitored.

122. (Original) The method of claim 116 wherein expression is measured with high density nucleic acid array.

123. (Original) The method of determining a pathological state of cells or tissues, comprising the steps of:

monitoring in a test sample comprising cells, expression of at least 10 mRNAs which are differentially expressed in cells which are normal and cells which are in the pathological state;

determining a pathological state of the cells of the test sample by matching the pattern of expression of the at least 10 mRNAs to a reference pattern determined for the pathological state.

124. (Original) The method of claim 123 wherein expression of at least 50 of said mRNAs is monitored.

125. (Original) The method of claim 123 wherein expression of at least 75 of said mRNAs is monitored.

126. (Original) The method of claim 123 wherein expression of at least 100 of said mRNAs is monitored.

127. (Original) The method of claim 123 wherein expression of at least 150 of said mRNAs is monitored.

128. (Original) The method of claim 123 wherein expression of at least 200 of said mRNAs is monitored.

129. (Original) The method of claim 123, wherein expression is measured with high density nucleic acid array.